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=> file .biotech
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
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FILE 'MEDLINE' ENTERED AT 09:44:04 ON 07 FEB 2005

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=> s gene (xa) express?
COMMAND INTERRUPTED
   3 FILES SEARCHED...
   4 FILES SEARCHED...
L1     1344038 GENE (XA) EXPRESS?
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=>

=> s gene (3a) express?
   4 FILES SEARCHED...
L2     1158464 GENE (3A) EXPRESS?

=> s component analysis
L3       22416 COMPONENT ANALYSIS

=> s l2 and l3
L4         523 L2 AND L3

=> s independent COMPONENT ANALYSIS
L5         802 INDEPENDENT COMPONENT ANALYSIS

=> s l2 and l5
L6          23 L2 AND L5

=> s l2 and l4
L7         523 L2 AND L4

=> s iterative
L8       27138 ITERATIVE

=> s l6 and l8
L9           0 L6 AND L8

=> dup rem
ENTER L# LIST OR (END):l6
PROCESSING COMPLETED FOR L6
L10         11 DUP REM L6 (12 DUPLICATES REMOVED)

=> d ibib abs l10 1-11
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L10 ANSWER 1 OF 11 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2004424264 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15247901
TITLE: **Independent component analysis** of microarray data in the study of endometrial cancer.
AUTHOR: Saidi Samir A; Holland Cathrine M; Kreil David P; MacKay David J C; Charnock-Jones D Stephen; Print Cristin G; Smith Stephen K
CORPORATE SOURCE: Department of Obstetrics and Gynaecology, University of Cambridge, Cambridge CB2 2SW, UK.. samsaidi@obgyn.cam.ac.uk
SOURCE: Oncogene, (2004 Aug 26) 23 (39) 6677-83.
Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200409
ENTRY DATE: Entered STN: 20040827
Last Updated on STN: 20040917
Entered Medline: 20040916

AB Gene microarray technology is highly effective in screening for differential **gene expression** and has hence become a popular tool in the molecular investigation of cancer. When applied to tumours, molecular characteristics may be correlated with clinical features such as response to chemotherapy. Exploitation of the huge amount of data generated by microarrays is difficult, however, and constitutes a major challenge in the advancement of this methodology. **Independent component analysis** (ICA), a modern statistical method, allows us to better understand data in such complex and noisy measurement environments. The technique has the potential to significantly increase the quality of the resulting data and improve the biological validity of subsequent analysis. We performed microarray experiments on 31 postmenopausal endometrial biopsies, comprising 11 benign and 20 malignant samples. We compared ICA to the established methods of principal component analysis (PCA), Cyber-T, and SAM. We show that ICA generated patterns that clearly characterized the malignant samples studied, in contrast to PCA. Moreover, ICA improved the biological validity of the genes identified as differentially expressed in endometrial carcinoma, compared to those found by Cyber-T and SAM. In particular, several genes involved in lipid metabolism that are differentially expressed in endometrial carcinoma were only found using this method. This report highlights the potential of ICA in the analysis of microarray data.

L10 ANSWER 2 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2005034636 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15662200
TITLE: Blind source separation and the analysis of microarray data.
AUTHOR: Chiappetta P; Roubaud M C; Torresani B
CORPORATE SOURCE: Laboratoire d'Analyse, Topologie et Probabilites, Centre de Mathematiques et Informatique, Universite de Provence, France.
SOURCE: Journal of computational biology : a journal of computational molecular cell biology, (2004) 11 (6) 1090-109.
Journal code: 9433358. ISSN: 1066-5277.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20050125
Last Updated on STN: 20050125

AB We develop an approach for the exploratory analysis of **gene**

expression data, based upon blind source separation techniques. This approach exploits higher-order statistics to identify a linear model for (logarithms of) expression profiles, described as linear combinations of "independent sources." As a result, it yields "elementary expression patterns" (the "sources"), which may be interpreted as potential regulation pathways. Further analysis of the so-obtained sources show that they are generally characterized by a small number of specific coexpressed or antiexpressed genes. In addition, the projections of the expression profiles onto the estimated sources often provides significant clustering of conditions. The algorithm relies on a large number of runs of "**independent component analysis**" with random initializations, followed by a search of "consensus sources." It then provides estimates for independent sources, together with an assessment of their robustness. The results obtained on two datasets (namely, breast cancer data and Bacillus subtilis sulfur metabolism data) show that some of the obtained gene families correspond to well known families of coregulated genes, which validates the proposed approach.

L10 ANSWER 3 OF 11 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2004544611 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15516835
TITLE: Bioinformatic analysis of primary endothelial cell gene array data illustrated by the analysis of transcriptome changes in endothelial cells exposed to VEGF-A and PlGF.
AUTHOR: Schoenfeld Jonathan; Lessan Khashayar; Johnson Nicola A; Charnock-Jones D Stephen; Evans Amanda; Vourvouhaki Ekaterini; Scott Laurie; Stephens Richard; Freeman Tom C; Saidi Samir A; Tom Brian; Weston Gareth C; Rogers Peter; Smith Stephen K; Print Cristin G
CORPORATE SOURCE: Department of Pathology, Cambridge University, Cambridge, UK.
SOURCE: Angiogenesis, (2004) 7 (2) 143-56.
Journal code: 9814575. ISSN: 0969-6970.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20041102
Last Updated on STN: 20041220

AB We recently published a review in this journal describing the design, hybridisation and basic data processing required to use gene arrays to investigate vascular biology (Evans et al. Angiogenesis 2003; 6: 93-104). Here, we build on this review by describing a set of powerful and robust methods for the analysis and interpretation of gene array data derived from primary vascular cell cultures. First, we describe the evaluation of transcriptome heterogeneity between primary cultures derived from different individuals, and estimation of the false discovery rate introduced by this heterogeneity and by experimental noise. Then, we discuss the appropriate use of Bayesian t-tests, clustering and **independent component analysis** to mine the data. We illustrate these principles by analysis of a previously unpublished set of gene array data in which human umbilical vein endothelial cells (HUVEC) cultured in either rich or low-serum media were exposed to vascular endothelial growth factor (VEGF)-A165 or placental growth factor (PlGF)-1(131). We have used Affymetrix U95A gene arrays to map the effects of these factors on the HUVEC transcriptome. These experiments followed a paired design and were biologically replicated three times. In addition, one experiment was repeated using serial analysis of **gene expression** (SAGE). In contrast to some previous studies, we found that VEGF-A and PlGF consistently regulated only small, non-overlapping and culture media-dependant sets of HUVEC transcripts, despite causing significant cell biological changes.

L10 ANSWER 4 OF 11 MEDLINE on STN

ACCESSION NUMBER: 2004130013 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15022635
TITLE: The operons, a criterion to compare the reliability of transcriptome analysis tools: ICA is more reliable than ANOVA, PLS and PCA.
AUTHOR: Carpentier Anne-Sophie; Riva Alessandra; Tisseur Pierre; Didier Gilles; Henaut Alain
CORPORATE SOURCE: Laboratoire Genome et Informatique, UMR 8116, Tour Evry2, 523 Place des Terrasses, 91034,Evry, France.. carpentier@genepole.cnrs.fr
SOURCE: Computational biology and chemistry, (2004 Feb) 28 (1) 3-10.
Journal code: 101157394. ISSN: 1476-9271.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200404
ENTRY DATE: Entered STN: 20040317
Last Updated on STN: 20040408
Entered Medline: 20040407

AB The number of statistical tools used to analyze transcriptome data is continuously increasing and no one, definitive method has so far emerged. There is a need for comparison and a number of different approaches has been taken to evaluate the effectiveness of the different statistical tools available for microarray analyses. In this paper, we describe a simple and efficient protocol to compare the reliability of different statistical tools available for microarray analyses. It exploits the fact that genes within an operon exhibit the same expression patterns. In order to compare the tools, the genes are ranked according to the most relevant criterion for each tool; for each tool we look at the number of different operons represented within the first twenty genes detected. We then look at the size of the interval within which we find the most significant genes belonging to each operon in question. This allows us to define and estimate the sensitivity and accuracy of each statistical tool. We have compared four statistical tools using Bacillus subtilis expression data: the analysis of variance (ANOVA), the principal component analysis (PCA), the **independent component analysis** (ICA) and the partial least square regression (PLS). Our results show ICA to be the most sensitive and accurate of the tools tested. In this article, we have used the protocol to compare statistical tools applied to the analysis of differential **gene expression**. However, it can also be applied without modification to compare the statistical tools developed for other types of transcriptome analyses, like the study of **gene** co-**expression**.

L10 ANSWER 5 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2003611185 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14673099
TITLE: Network component analysis: reconstruction of regulatory signals in biological systems.
AUTHOR: Liao James C; Boscolo Riccardo; Yang Young-Lyeol; Tran Linh My; Sabatti Chiara; Roychowdhury Vwani P
CORPORATE SOURCE: Departments of Chemical Engineering, University of California, Los Angeles, CA 90095, USA.. liaoj@ucla.edu
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2003 Dec 23) 100 (26) 15522-7.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200404
ENTRY DATE: Entered STN: 20031225

Last Updated on STN: 20040421
Entered Medline: 20040420

AB High-dimensional data sets generated by high-throughput technologies, such as DNA microarray, are often the outputs of complex networked systems driven by hidden regulatory signals. Traditional statistical methods for computing low-dimensional or hidden representations of these data sets, such as principal component analysis and **independent component analysis**, ignore the underlying network structures and provide decompositions based purely on a priori statistical constraints on the computed component signals. The resulting decomposition thus provides a phenomenological model for the observed data and does not necessarily contain physically or biologically meaningful signals. Here, we develop a method, called network component analysis, for uncovering hidden regulatory signals from outputs of networked systems, when only a partial knowledge of the underlying network topology is available. The a priori network structure information is first tested for compliance with a set of identifiability criteria. For networks that satisfy the criteria, the signals from the regulatory nodes and their strengths of influence on each output node can be faithfully reconstructed. This method is first validated experimentally by using the absorbance spectra of a network of various hemoglobin species. The method is then applied to microarray data generated from yeast Saccharamyces cerevisiae and the activities of various transcription factors during cell cycle are reconstructed by using recently discovered connectivity information for the underlying transcriptional regulatory networks.

L10 ANSWER 6 OF 11 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN DUPLICATE 3

ACCESSION NUMBER: 2003:474219 BIOSIS
DOCUMENT NUMBER: PREV200300474219
TITLE: Reproducibility assessment of **independent component analysis** of expression ratios from DNA microarrays.
AUTHOR(S): Kreil, David Philip [Reprint Author]; MacKay, David J. C.
CORPORATE SOURCE: Department of Genetics, University of Cambridge, Downing Street, Cambridge, CB2 3EH, UK
kreil@ebi.ac.uk
SOURCE: Comparative and Functional Genomics, (June 2003) Vol. 4, No. 3, pp. 300-317. print.
ISSN: 1531-6912 (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 15 Oct 2003
Last Updated on STN: 15 Oct 2003

AB DNA microarrays allow the measurement of transcript abundances for thousands of genes in parallel. Most commonly, a particular sample of interest is studied next to a neutral control, examining relative changes (ratios). **Independent component analysis** (ICA) is a promising modern method for the analysis of such experiments. The condition of ICA algorithms can, however, depend on the characteristics of the data examined, making algorithm properties such as robustness specific to the given application domain. To address the lack of studies examining the robustness of ICA applied to microarray measurements, we report on the stability of variational Bayesian ICA in this domain. Microarray data are usually preprocessed and transformed. Hence we first examined alternative transforms and data selections for the smallest modelling reconstruction errors. Log-ratio data are reconstructed better than non-transformed ratio data by our linear model with a Gaussian error term. To compare ICA results we must allow for ICA invariance under rescaling and permutation of the extracted signatures, which hold the loadings of the original variables (gene transcript ratios) on particular latent variables. We introduced a method to optimally match corresponding signatures between sets of results. The stability of signatures was then examined after (1) repetition of the same analysis run

with different random number generator seeds, and (2) repetition of the analysis with partial data sets. The effects of both dropping a proportion of the gene transcript ratios and dropping measurements for several samples have been studied. In summary, signatures with a high relative data power were very likely to be retained, resulting in an overall stability of the analyses. Our analysis of 63 yeast wild-type vs. wild-type experiments, moreover, yielded 10 reliably identified signatures, demonstrating that the variance observed is not just noise.

L10 ANSWER 7 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2003533690 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14611662
TITLE: Application of **independent component analysis** to microarrays.
AUTHOR: Lee Su-In; Batzoglou Serafim
CORPORATE SOURCE: Department of Computer Science, Stanford University, Stanford, CA94305-9010, USA.
SOURCE: Genome biology, (2003) 4 (11) R76.
Journal code: 100960660. ISSN: 1465-6914.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200403
ENTRY DATE: Entered STN: 20031113
Last Updated on STN: 20040309
Entered Medline: 20040308

AB We apply linear and nonlinear **independent component analysis** (ICA) to project microarray data into statistically independent components that correspond to putative biological processes, and to cluster genes according to over- or under-expression in each component. We test the statistical significance of enrichment of gene annotations within clusters. ICA outperforms other leading methods, such as principal component analysis, k-means clustering and the Plaid model, in constructing functionally coherent clusters on microarray datasets from Saccharomyces cerevisiae, Caenorhabditis elegans and human.

L10 ANSWER 8 OF 11 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2003032008 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12490446
TITLE: A decomposition model to track **gene expression** signatures: preview on observer-independent classification of ovarian cancer.
AUTHOR: Martoglio Ann-Marie; Miskin James W; Smith Stephen K; MacKay David J C
CORPORATE SOURCE: Department of Pathology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK.. amm53@cam.ac.uk
SOURCE: Bioinformatics (Oxford, England), (2002 Dec) 18 (12) 1617-24.
Journal code: 9808944. ISSN: 1367-4803.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200307
ENTRY DATE: Entered STN: 20030124
Last Updated on STN: 20030703
Entered Medline: 20030702

AB MOTIVATION: A number of algorithms and analytical models have been employed to reduce the multidimensional complexity of DNA array data and attempt to extract some meaningful interpretation of the results. These include clustering, principal components analysis, self-organizing maps,

and support vector machine analysis. Each method assumes an implicit model for the data, many of which separate genes into distinct clusters defined by similar expression profiles in the samples tested. A point of concern is that many genes may be involved in a number of distinct behaviours, and should therefore be modelled to fit into as many separate clusters as detected in the multidimensional **gene expression** space. The analysis of **gene expression** data using a decomposition model that is independent of the observer involved would be highly beneficial to improve standard and reproducible classification of clinical and research samples. RESULTS: We present a variational **independent component analysis** (ICA) method for reducing high dimensional DNA array data to a smaller set of latent variables, each associated with a gene signature. We present the results of applying the method to data from an ovarian cancer study, revealing a number of tissue type-specific and tissue type-independent gene signatures present in varying amounts among the samples surveyed. The observer independent results of such molecular analysis of biological samples could help identify patients who would benefit from different treatment strategies. We further explore the application of the model to similar high-throughput studies.

L10 ANSWER 9 OF 11 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 2002116677 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11836211
TITLE: Linear modes of **gene expression** determined by **independent component analysis**.
AUTHOR: Liebermeister Wolfram
CORPORATE SOURCE: Theoretische Biophysik, Institut fur Biologie, Humboldt-Universitat zu Berlin, Invalidenstrasse 42, 10115 Berlin, Germany.. wolfram.liebermeister@rz-hu-berlin.de
SOURCE: Bioinformatics (Oxford, England), (2002 Jan) 18 (1) 51-60. Journal code: 9808944. ISSN: 1367-4803.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020220
Last Updated on STN: 20020611
Entered Medline: 20020610

AB MOTIVATION: The expression of genes is controlled by specific combinations of cellular variables. We applied **Independent Component Analysis** (ICA) to **gene expression** data, deriving a linear model based on hidden variables, which we term 'expression modes'. The **expression** of each **gene** is a linear function of the expression modes, where, according to the ICA model, the linear influences of different modes show a minimal statistical dependence, and their distributions deviate sharply from the normal distribution. RESULTS: Studying cell cycle-related **gene expression** in yeast, we found that the dominant expression modes could be related to distinct biological functions, such as phases of the cell cycle or the mating response. Analysis of human lymphocytes revealed modes that were related to characteristic differences between cell types. With both data sets, the linear influences of the dominant modes showed distributions with large tails, indicating the existence of specifically up- and downregulated target genes. The expression modes and their influences can be used to visualize the samples and genes in low-dimensional spaces. A projection to expression modes helps to highlight particular biological functions, to reduce noise, and to compress the data in a biologically sensible way.

L10 ANSWER 10 OF 11 EMBASE
on STN

ACCESSION NUMBER: 2002367756 EMBASE
TITLE: Correlation of **gene expression** profiles with clinical data.
AUTHOR: Stratowa C.
CORPORATE SOURCE: Dr. C. Stratowa, Boehringer-Ingelheim Austria GmbH, Department of NCE Discovery, Dr Boehringergasse 5-11, A-1121 Vienna, Austria. christian.stratowa@vie.boehringerin gelheim.com
SOURCE: Current Drug Discovery, (1 Sep 2002) -/SEPT. (29-33). ISSN: 1472-7463 CODEN: CDDUAI
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Recent advances in expression profiling technologies now allow the study of **gene expression** and disease-related changes on a genome-wide scale. However, the quality of information obtained from expression profile data alone is limited. In contrast, correlation of expression profiles with a variety of clinical parameters should allow a more extensive analysis. The major challenge is the complexity of these datasets, which necessitates the use of sophisticated statistical algorithms, and the extraction of biological knowledge.

L10 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:489877 CAPLUS
DOCUMENT NUMBER: 137:363847
TITLE: Blind gene classification - an application of a signal separation method
AUTHOR(S): Hori, Gen; Nishimura, Shin-ichi; Inoue, Masato; Nakahara, Hiroyuki
CORPORATE SOURCE: Laboratory for Advanced Brain Signal Processing, Brain Science Institute, Wako-shi, Saitama, 351-0198, Japan
SOURCE: Genome Informatics Series (2001), 12, 255-256 CODEN: GINSE9; ISSN: 0919-9454
PUBLISHER: Universal Academy Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A new method based on independent component anal. (ICA) is shown to be a promising approach to automatic gene classification. Although ICA is similar to principal component anal. (PCA), ICA has some advantage to PCA because it exploits higher order statistics and has no restriction to orthogonal transformations. The validity of the new method is illustrated by application to previously published yeast sporulation **gene expression** data. The data consists of expression data of 6118 genes in yeast genome which were sampled at seven different times during sporulation. The classified groups by the ICA-based method have a good match with the classified groups based on manually obtained model profiles. It is notable that ICA-based method does not require a domain knowledge on genome and automatically classifies genes without any manual labor.
REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 09:44:04 ON

07 FEB 2005

L1	1344038	S	GENE (XA) EXPRESS?
L2	1158464	S	GENE (3A) EXPRESS?
L3	22416	S	COMPONENT ANALYSIS
L4	523	S	L2 AND L3
L5	802	S	INDEPENDENT COMPONENT ANALYSIS
L6	23	S	L2 AND L5
L7	523	S	L2 AND L4
L8	27138	S	ITERATIVE
L9	0	S	L6 AND L8
L10	11		DUP REM L6 (12 DUPLICATES REMOVED)

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	5	gene near expressin	USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/07 10:03
L2	46612	gene near express$	USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/07 10:04
L3	2984	component adj analysis	USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/07 10:04
L4	80	l2 and l3	USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/07 10:05
L5	660058	independent adj component analysis	USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/07 10:05
L6	122	independent adj component adj analysis	USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/07 10:05
L7	3	l4 and l6	USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/07 10:05

US 6816743 B2 USPAT	US 6171787 B1 USPAT
US 6789069 B1 USPAT	US 6165734 A USPAT
US 6770435 B1 USPAT	US 6156576 A USPAT
US 6760715 B1 USPAT	US 6130043 A USPAT
US 6759200 B1 USPAT	US 6110675 A USPAT
US 6750036 B2 USPAT	US 6103199 A USPAT
US 6743576 B1 USPAT	US 6066459 A USPAT
US 6738716 B1 USPAT	US 6055325 A USPAT
US 6728642 B2 USPAT	US 6051559 A USPAT
US 6728396 B2 USPAT	US 6015670 A USPAT
US 6727406 B2 USPAT	US 6007996 A USPAT
US 6714925 B1 USPAT	US 5994075 A USPAT
US 6713257 B2 USPAT	US 5952180 A USPAT
US 6696545 B1 USPAT	US 5939265 A USPAT
US 6683455 B2 USPAT	US 5936731 A USPAT
US 6678413 B1 USPAT	US 5929223 A USPAT
US 6673908 B1 USPAT	US 5919638 A USPAT
US 6664062 B1 USPAT	US 5817462 A USPAT
US 6660834 B2 USPAT	US 5814454 A USPAT
US 6651008 B1 USPAT	US 5804386 A USPAT
US 6631331 B1 USPAT	US 5764819 A USPAT
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